

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- 5 (i) APPLICANT:  
(A) NAME: Koninklijke Universiteit Nijmegen.  
Afdeling tumorimmunologie  
(B) STREET: Philips van Leydenlaan 25  
(C) CITY: Nijmegen  
10 (E) COUNTRY: Netherlands  
(F) POSTAL CODE (ZIP): 6525 EX  
(G) TELEPHONE: + 31 243 617 600  
(H) TELEFAX: + 31 243 540 339
- 15 (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
20 (D) SOFTWARE: PatentIn Release #1.0. Version #1.30
- (ii) TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING  
DENDRITIC CELL-T CELL INTERACTION
- 25 (iii) NUMBER OF SEQUENCES: 2

## (2) INFORMATION FOR SEQ ID NO:1:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1215 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- 40 (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- |    |   |     |
|----|---|-----|
| 45 | ATGAGTGACT CCAAGGAACC AAGACTGCAG CAGCTGGGCC TCCTGGAGGA GGAACAGCTG | 60  |
|    | AGAGGCCTTG GATTCCGACA GACTCGAGGA TACAAGAGCT TAGCAGGGTG TCTTGGCCAT | 120 |
|    | GGTCCCCTGG TGCTGCAACT CCTCTCCTTC ACGCTCTTGG CTGGGCTCCT TGTCCAAGTG | 180 |
| 50 | TCCAAGGTCC CCAGCTCCAT AAGTCAGGAA CAATCCAGGC AAGACGCGAT CTACCAGAAC | 240 |
|    | CTGACCCAGC TTAAAGCTGC AGTGGGTGAG CTCTCAGAGA AATCCAAGCT GCAGGAGATC | 300 |
| 55 | TACCAGGAGC TGACCCAGCT GAAGGCTGCA GTGGGTGAGC TTCCAGAGAA ATCTAAGCTG | 360 |

CAGGAGATCT ACCAGGAGCT GACCCGGCTG AAGGCTGCAG TGGGTGAGCT TCCAGAGAAA 420  
 TCTAAGCTGC AGGAGATCTA CCAGGAGCTG ACCTGGCTGA AGGCTGCAGT GGGTGAGCTT 480  
 5 CCAGAGAAAT CTAAGATGCA GGAGATCTAC CAGGAGCTGA CTCGGCTGAA GGCTGCAGTG 540  
 GGTGAGCTTC CAGAGAAATC TAAGCAGCAG GAGATCTACC AGGAGCTGAC CCGGCTGAAG 600  
 10 GCTGCAGTGG GTGAGCTTCC AGAGAAATCT AAGCAGCAGG AGATCTACCA GGAGCTGACC 660  
 CGGCTGAAGG CTGCAGTGGG TGAGCTTCCA GAGAAATCTA AGCAGCAGGA GATCTACCAG 720  
 GAGCTGACCC AGCTGAAGGC TGCAGTGGAA CGCCTGTGCC ACCCCTGTCC CTGGGAATGG 780  
 15 ACATTCTTCC AAGGAAACTG TTACTTCATG TCTAACTCCC AGCGGAACTG GCACGACTCC 840  
 ATCACC GCCT GCAAAGAAGT GGGGGCCCAG CTCGTCGTAA TCAAAAGTGC TGAGGAGCAG 900  
 20 AACTTCCTAC AGCTGCAGTC TTCCAGAAGT AACCGCTTCA CCTGGATGGG ACTTTCAGAT 960  
 CTAAATCAGG AAGGCACGTG GCAATGGGTG GACGGCTCAC CTCTGTTGCC CAGCTTCAAG 1020  
 CAGTATTGGA ACAGAGGAGA GCCCAACAAC GTTGGGGAGG AAGACTGCGC GGAATTTAGT 1080  
 25 GGCAATGGCT GGAACGACGA CAAATGTAAT CTTGCCAAAT TCTGGATCTG CAAAAAGTCC 1140  
 GCAGCCTCCT GCTCCAGGGA TGAAGAACAG TTTCTTTCTC CAGCCCCTGC CACCCCAAAC 1200  
 30 CCCCCTCCTG CGTAG 1215

2) INFORMATION FOR SEQ ID NO:2:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 415 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

45 Met Ser Asp Ser Lys Glu Pro Arg Leu Gln Gln Leu Gly Leu Leu  
     1                    5                    10                    15  
 Glu Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly  
                     20                    25                    30  
 50 Tyr Lys Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu  
                     35                    40                    45  
 55 Gln Leu Leu Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val  
                     50                    55                    60

	Ser	Lys	Val	Pro	Ser <sub>65</sub>	Ser	Ile	Ser	Gln	Glu <sub>70</sub>	Gln	Ser	Arg	Gln	Asp <sub>75</sub>
5	Ala	Ile	Tyr	Gln	Asn <sub>80</sub>	Leu	Thr	Gln	Leu	Lys <sub>85</sub>	Ala	Ala	Val	Gly	Glu <sub>90</sub>
	Leu	Ser	Glu	Lys	Ser <sub>95</sub>	Lys	Leu	Gln	Glu	Ile <sub>100</sub>	Tyr	Gln	Glu	Leu	Thr <sub>105</sub>
10	Gln	Leu	Lys	Ala	Ala <sub>110</sub>	Val	Gly	Glu	Leu	Pro <sub>115</sub>	Glu	Lys	Ser	Lys	Leu <sub>120</sub>
	Gln	Glu	Ile	Tyr	Gln <sub>125</sub>	Glu	Leu	Thr	Arg	Leu <sub>130</sub>	Lys	Ala	Ala	Val	Gly <sub>135</sub>
15	Glu	Leu	Pro	Glu	Lys <sub>140</sub>	Ser	Lys	Leu	Gln	Glu <sub>145</sub>	Ile	Tyr	Gln	Glu	Leu <sub>150</sub>
20	Thr	Trp	Leu	Lys	Ala <sub>155</sub>	Ala	Val	Gly	Glu	Leu <sub>160</sub>	Pro	Glu	Lys	Ser	Lys <sub>165</sub>
	Met	Gln	Glu	Ile	Tyr <sub>170</sub>	Gln	Glu	Leu	Thr	Arg <sub>175</sub>	Leu	Lys	Ala	Ala	Val <sub>180</sub>
25	Gly	Glu	Leu	Pro	Glu <sub>185</sub>	Lys	Ser	Lys	Gln	Gln <sub>190</sub>	Glu	Ile	Tyr	Gln	Glu <sub>195</sub>
	Leu	Thr	Arg	Leu	Lys <sub>200</sub>	Ala	Ala	Val	Gly	Glu <sub>205</sub>	Leu	Pro	Glu	Lys	Ser <sub>210</sub>
30	Lys	Gln	Gln	Glu	Ile <sub>215</sub>	Tyr	Gln	Glu	Leu	Thr <sub>220</sub>	Arg	Leu	Lys	Ala	Ala <sub>225</sub>
35	Val	Gly	Glu	Leu	Pro <sub>230</sub>	Glu	Lys	Ser	Lys	Gln <sub>235</sub>	Gln	Glu	Ile	Tyr	Gln <sub>240</sub>
	Glu	Leu	Thr	Gln	Leu <sub>245</sub>	Lys	Ala	Ala	Val	Glu <sub>250</sub>	Arg	Leu	Cys	His	Pro <sub>255</sub>
40	Cys	Pro	Trp	Glu	Trp <sub>260</sub>	Thr	Phe	Phe	Gln	Gly <sub>265</sub>	Asn	Cys	Tyr	Phe	Met <sub>270</sub>
45	Ser	Asn	Ser	Gln	Arg <sub>275</sub>	Asn	Trp	His	Asp	Ser <sub>280</sub>	Ile	Thr	Ala	Cys	Lys <sub>285</sub>
	Glu	Val	Gly	Ala	Gln <sub>290</sub>	Leu	Val	Val	Ile	Lys <sub>295</sub>	Ser	Ala	Glu	Glu	Gln <sub>300</sub>
50	Asn	Phe	Leu	Gln	Leu <sub>305</sub>	Gln	Ser	Ser	Arg	Ser <sub>310</sub>	Asn	Arg	Phe	Thr	Trp <sub>315</sub>
55	Met	Gly	Leu	Ser	Asp <sub>320</sub>	Leu	Asn	Gln	Glu	Gly <sub>325</sub>	Thr	Trp	Gln	Trp	Val <sub>330</sub>

Asp Gly Ser Pro Leu Leu Pro Ser Phe Lys Gln Tyr Trp Asn Arg  
335 340 345

5 Gly Glu Pro Asn Asn Val Gly Glu Glu Asp Cys Ala Glu Phe Ser  
350 355 360

Gly Asn Gly Trp Asn Asp Asp Lys Cys Asn Leu Ala Lys Phe Trp  
365 370 375

10 Ile Cys Lys Lys Ser Ala Ala Ser Cys Ser Arg Asp Glu Glu Gln  
380 385 390

Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn Pro Pro Pro Ala \*

15 395 400 404